

SEQ. ALIGNMENT
DATA: please Scan & mail.

181 MLTFLFAERGDPDRGKSDQLDALLWRAERPGSPWSPGGRPGHVECSAIALTRIG 240
241 TGLDIQGGSDLIFFPHHYSAAHESVTGERFARHYVHTGMIGWDHMKSRGNLV 300
241 TGLDIQGGSDLIFFPHHYSAAHESVTGERFARHYVHTGMIGWDHMKSRGNLV 300
301 SOLRAQGVDPBSAIRLGLFSGHYREDRFSNEVLDEANARLARWSATALPEAPDATDVIA 360
301 SOLRAQGVDPBSAIRLGLFSGHYREDRFSNEVLDEANARLARWSATALPEAPDATDVIA 360
361 RVROQLADDDLTTPKALAALDGCWCTDALSYGCHDTPSRIVATTVDALLGVDL 412
361 RVROQLADDDLTTPKALAALDGCWCTDALSYGCHDTPSRIVATTVDALLGVDL 412

RESULT 2
US-10-934-893-3251
; Sequence 3251, Application US/10934893
; Publication No. US20070042383A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek, Bannantine, John P., Li, Ling-Ling, Zhang, Qing, and
; APPLICANT: Amosin, Alongkorn
; TITLE OF INVENTION: Mycobacterial Diagnostics
; FILE REFERENCE: 09531/112002
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/IB2003/006509
; PRIOR FILING DATE: 2003-03-06
; PRIOR FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 5809
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3251
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Mycobacterium paratuberculosis
US-10-934-893-3251

Query Match 82.4%; Score 1808.5; DB 5; Length 415;
Best Local Similarity 79.6%; Pred. No. 8.5e-164;
Matches 331; Conservative 38; Mismatches 42; Indels 5; Gaps 2;
1 MQSWSPAPVVPVPGRGPALRFLDSADQVRPVT---PGPTATWVCGITPYDATHLCHA 56
1 MRSSSPQVQLPGRGPELALYDTSRQVRPVAAGAGPGSAATWVCGITPYDATHLCHA 60
57 ATYTLFVLHRLWLDAGHTVOYVQNVTDVDDPLFERAERDGDIDWRTLGDRQTQLPREDMA 116
61 ATYLAFLDIYRQWLGLDGHVYQNVTDVDDPLFERAARDGVDWALAEVSLFREDMA 120
117 ALRVLPDHYVAATAIAEVVEMVEKLLASGAAYIVBDAEYDPVYFRADATQFGYESGY 176
121 ALRILAPDYVGAATAIADVVELVEKMLASGAAYV-DGEFFDIYFRADATQFGYESGY 179
177 DRDTMLTLFAERGDPDRPGKSDQLDALLWRAERPGSPWSPGGRPGHVECSAIAL 236
180 DRETMLRLFAERGDPDRPGKSDQLDALLWRAERPGSPWSPGGRPGHVECSAIAL 239
237 TRIGTGLDIQGGSDLIFFPHHYSAAHESVTGERFARHYVHTGMIGWDHMKSRGN 296
240 SRIGGLDIQGGSDLIFFPHHEFTAAHAECVGERRERFARHYVHTGMIGWDHMKSRGN 299
297 LVLSQLRAQGVDPBSAIRLGLFSGHYREDRFSNEVLDEANARLARWSATALPEAPDAT 356
300 LVLSQLRAQGVDPBSAIRLGLFSGHYREDRFSNEVLDEANARLARWSATALPEAPDAT 359
357 DVITARVQYLAADDLTTPKALAALDGCWCTDALSYGCHDTPSRIVATTVDALLGVDL 412
360 DVITARVQYLAADDLTTPKALAALDGCWCTDALSYGCHDTPSRIVATTVDALLGVDL 415

RESULT 3
US-10-511-244-4
; Sequence 4, Application US/10511244
; Publication No. US20060183116A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA
; APPLICANT: SAREEN, Dipati
; APPLICANT: NEWTON, Gerald L.
; APPLICANT: FAHEY, Robert C.
; APPLICANT: BUCHMEIER, Nancy
; APPLICANT: STEFFEK, Micah
; APPLICANT: AV-GAY, Yossef
; APPLICANT: RAWAT, Mamta
; APPLICANT: KOLEDIN, Teresa
; TITLE OF INVENTION: METHODS OF USE OF THE ENZYMES OF MYCOTHIOL SYNTHESIS
; FILE REFERENCE: UCSDI420-1
; CURRENT FILING DATE: 2004-10-13
; PRIOR APPLICATION NUMBER: PCT/US 03/11539
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 60/373,890
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/373,079
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-511-244-4

Query Match 82.2%; Score 1803; DB 5; Length 414;
Best Local Similarity 79.0%; Pred. No. 2.8e-163;
Matches 327; Conservative 37; Mismatches 48; Indels 2; Gaps 1;
1 MQSWSPAPVVPVPGRGPALRFLDSADQVRPVT---PGPTATWVCGITPYDATHLCHAATYL 60
1 MQSWCPFPVLPVPGRGPALRFLDSADQVRPVAAGAGPGSAATWVCGITPYDATHLCHAATYL 60
61 TFDLVHRLWLDAGHTVOYVQNVTDVDDPLFERAERDGDIDWRTLGDRQTQLPREDMAALRV 120
61 TFDLVHRLWLDAGHTVOYVQNVTDVDDPLFERAERDGDIDWRTLGDRQTQLPREDMAALRV 120
121 LPPDHYVAATAIAEVVEMVEKLLASGAAYIV-BDAEYDPVYFRADATQFGYESGYDR 178
121 LPPDHYVAATAIAEVVEMVEKLLASGAAYIV-BDAEYDPVYFRADATQFGYESGYDR 180
179 DTMLTLFAERGDPDRPGKSDQLDALLWRAERPGSPWSPGGRPGHVECSAIALTR 238
181 DTMLTLFAERGDPDRPGKSDQLDALLWRAERPGSPWSPGGRPGHVECSAIALTR 240
239 ICTGLDIQGGSDLIFFPHHYSAAHESVTGERFARHYVHTGMIGWDHMKSRGNLV 298
241 IGSGGLDIQGGSDLIFFPHHEFTAAHAECVGERRERFARHYVHTGMIGWDHMKSRGNLV 300
299 LVLSQLRAQGVDPBSAIRLGLFSGHYREDRFSNEVLDEANARLARWSATALPEAPDATDV 358
301 LVLSQLRAQGVDPBSAIRLGLFSGHYREDRFSNEVLDEANARLARWSATALPEAPDATDV 360
359 IARVQYLAADDLTTPKALAALDGCWCTDALSYGCHDTPSRIVATTVDALLGVDL 412
361 VARVRYLAADDLTTPKALAALDGCWCTDALSYGCHDTPSRIVATTVDALLGVDL 414

RESULT 4
US-11-041-504-288
; Sequence 288, Application US/11041504
; Publication No. US20070161091A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
0040
0132
1013

APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oekar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN GENETIC STABILITY, GENE EXPRESSION,
TITLE OF INVENTION: AND PROTEIN SECRETION AND FOLDING
FILE REFERENCE: BGI-127CF
CURRENT APPLICATION NUMBER: US/11/041,504
CURRENT FILING DATE: 2005-01-21
PRIOR APPLICATION NUMBER: US/09/602,839
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/143752
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: 60/151671
PRIOR FILING DATE: 1999-08-08
PRIOR APPLICATION NUMBER: DE 19931412.8
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932928.1
PRIOR FILING DATE: 1999-07-14
NUMBER OF SEQ ID NOS: 618
SEQ ID NO 288
LENGTH: 420
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-11-041-504-288

Query Match 59.7%; Score 1309; DB 6; Length 420;
Best Local Similarity 59.7%; Pred. No. 5.8e-116;
Matches 253; Conservative 47; Mismatches 108; Indels 16; Gaps 4;

Qy 1 MQSASPAIPVPPGPGALRFDSDADROVRVTPGPTAT-----MYVCGITPYDATHLGH 55
Db 1 MQSPTTEVPALACTPVPLEFDTADQEVRLVETPPAGSDTPVGMVCGITPYDSTHLGH 60
Qy 56 AATYLTDLVRLWLDAGHTVQYVQNTVDVDDPLFERAERDGDWRTLGDRDTOLFRDM 115
Db 61 AATYLAFDLIYRLLDNDHDVHYVQNTVDVDDPLFERAARDGVDWDLGTSQINLFRSDM 120
Qy 116 AALRVLPDHYVAATDAIEAEMVEKLLASGAAYIVEDAEYDPVFRADATAGFYESG 175
Db 121 EALSIIIPKQYGAIESIDEIEMVKTLLDEGAAYIVEDAEYDPVFRADATAGFYESN 180
Qy 176 YDRDTMTLTPAERGGDPRCKSDQLDALLWRAERPGEPSPFGRGPGHVECSAIA 235
Db 181 YDAATMAEFAERGGDPRCKSDQLDALLWRAERPGEPSPFGRGPGHVECSAIA 240
Qy 236 LTRIGTGLDIQGGSDLIFFPHHEYSAAHAESVTGERFARHYVHTGMIGDGHKMSKRG 295
Db 241 TNRIGHSFDIQGGSDLIFFPHHEYSAAHAESVTGERFARHYVHTGMIGDGHKMSKRG 300
Qy 296 NLVLSQRAQGVDPSPAIRLGLFSGHYREDRFWSNEVLDEANARLARWR-SATALPEAPD 354
Db 301 NLEPVSLTAAGHEPGALRGVFNHYGRNDRNDAESLATAEORLATWREARAATNRD 360
Qy 355 ATDVIAVRQVLAADLTPKALALDGC-----TDALSYGGHDTESPRLVATVVDALL 408
Db 361 AIATVEQLRAHLSADLTGPGALAAVDNWAAGIDTTTDSKEF-----TEVGNIVVAIDALL 416
Qy 409 GVDL 412
Db 417 GVQL 420

RESULT 5
US-09-738-626-5170
; Sequence 5170, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIKOGUCHI, HIROSHI

APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 5170
LENGTH: 404
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-5170

Query Match 57.8%; Score 1269; DB 3; Length 404;
Best Local Similarity 60.6%; Pred. No. 3.7e-112;
Matches 246; Conservative 45; Mismatches 99; Indels 16; Gaps 4;

Qy 19 LRLPDSADROVRVTPGPTAT-----MYVCGITPYDATHLGHAAATVLTDLVRLWLDAG 73
Db 3 LELEFDTADQEVRLVETPPAGSDTPVGMVCGITPYDSTHLGHAAATVLAFLIYRLLDND 62
Qy 74 HTVQVQNTVDVDDPLFERAERDGDWRTLGDRDTOLFRDMALRVLPDHYVAATDAI 133
Db 63 HDVHYVQNTVDVDDPLFERAARDGVDWDLGTSQINLFRSDMEALSIIIPKQYGAIESI 122
Qy 134 AEVEMVEKLLASGAAYIVEDAEYDPVFRADATAGFYESGYDRDTMTLTPAERGGD 193
Db 123 DEVIEMVKTLLDEGAAYIVEDAEYDPVFRADATAGFYESGYDRDTMTLTPAERGGD 182
Qy 194 RPKSDQLDALLWRAERPGEPSPFGRGPGHVECSAIAITRIGTGLDIQGGSDLI 253
Db 183 RPKKXNPMDALIWRAREGEPSPFGRGPGHVECSAIAITRIGTGLDIQGGSDLI 242
Qy 254 FPHHEYSAAHAESVTGERFARHYVHTGMIGDGHKMSKRGNLVLSQRAQGVDPSPAI 313
Db 243 FPHHEFSAAHAESVTGERFARHYVHTGMIGDGHKMSKRGNLVLSQRAQGVDPSPAI 302
Qy 314 RLGLFSGHYREDRFWSNEVLDEANARLARWR-SATALPEAPDADTVIARVQYLAADLDT 372
Db 303 RLGVFNHYGRNDRNDAESLATAEORLATWREARAATNRDIAIVVEQLRAHLSADLDT 362
Qy 373 PKALALDGC-----TDALSYGGHDTESPRLVATVVDALLGVDL 412
Db 363 PGALAAVDNWAAGIDTTTDSKEF-----TEVGNIVVAIDALLGVQL 404

RESULT 6
US-10-805-394-5170
; Sequence 5170, Application US/10805394
; Publication No. US20060228712A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIKOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO

; APPLICANT: OZAKI, AKIO
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-125
 ; CURRENT APPLICATION NUMBER: US/10/805,394
 ; CURRENT FILING DATE: 2004-03-22
 ; PRIOR APPLICATION NUMBER: JP 99/377484
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: JP 00/159162
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: JP 00/280988
 ; PRIOR FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 7059
 ; SOFTWARE: PatentIn ver. 3.0
 ; SEQ ID NO 5170
 ; LENGTH: 404
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 US-10-805-394-5170

Query Match 57.8%; Score 1269; DB 5; Length 404;
 Best Local Similarity 60.6%; Pred. No. 3.7e-112;
 Matches 246; Conservative 45; Mismatches 99; Indels 16; Gaps 4;

Qy	19	LRLPDSADQVRPVTPPGTAT-----MVCGITPYDATHLGHAAATYLTFLVHRLWLDAG 73
Db	3	LELFDTADQEVRLVETPPAGSDTPVGMVCGITPYDSTHLGHAAATYLAFLDIYRILLND 62
Qy	74	HTVQVQNVTVDDPLFERAERDGDWRTGLDRETQLFREDMAALRVLPVHDYVAATDAI 133
Db	63	HDVHYVQNVITDVPDLFERAARDGVDRLDGTSLQINLFRSDMEALSIIIPKDIYGAIESI 122
Qy	134	AEVMEVEKLASGAAYIVEDAEYDPVYFRADATAQPGYESGYDRDTMLTLFAERGGDDP 193
Db	123	DEVIMWTKLLDEGAAYIVEDAEYDPVYASINATDKFGYESYDAATMAEFPAERGGDPE 182
Qy	194	RPKSDQDALLWRAERGPSPFGRGRPGHVECSAIALTRIGTGLDIQGGSDLI 253
Db	183	RPKKNPMDALLWRAAREGEPSWESPFGRGPGHVECSAIALTRNLGHISFDIQGGSDLI 242
Qy	254	PPHYESAAHAEVYTGERRFAHYHTGMIGWDGKMSKSRGNLVLVSOLRAQGVDPSPAI 313
Db	243	PPHFEFSAHAHAANGVERMAHYHAGMISQGVKMSKSLNLFSEVSLTAAGHEPGAI 302
Qy	314	RLGLFSGHYREDRFSNEVLDEANARLARWR-SATALPEAPDATDVIAVRQYRLADDDLT 372
Db	303	RLGVFANYHRYGNDNAESLATAEQRLATWREARAATNREDAIAVVEQLRAHLSADLDT 362
Qy	373	PKAALALDGC-----TDALSYGGHDTSPRLVATTVALLGVDL 412
Db	363	PGALAAVDNWAAGIDTTTDSKEF-----TEVGNIVVAAIDALLGVQL 404

RESULT 7
 US-10-511-244-6
 ; Sequence 6, Application US/10511244
 ; Publication No. US20060183116A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
 ; APPLICANT: SAREEN, Dipti
 ; APPLICANT: NEWTON, Gerald L.
 ; APPLICANT: FAHEY, Robert C.
 ; APPLICANT: BUCHMEIER, Nancy
 ; APPLICANT: STEFFEK, Micah
 ; APPLICANT: AV-GAY, Yossef
 ; APPLICANT: RAWAT, Mamta
 ; APPLICANT: KOLEDIN, Teresa
 ; TITLE OF INVENTION: METHODS OF USE OF THE ENZYMES OF MYCOTHOLIOL SYNTHESIS
 ; FILE REFERENCE: UCSD1420-1
 ; CURRENT APPLICATION NUMBER: US/10/511,244
 ; CURRENT FILING DATE: 2004-10-13
 ; PRIOR APPLICATION NUMBER: PCT/US 03/11539
 ; PRIOR FILING DATE: 2003-04-15

; PRIOR APPLICATION NUMBER: US 60/373,890
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: US 60/373,079
 ; PRIOR FILING DATE: 2002-04-15
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 409
 ; TYPE: PRT
 ; ORGANISM: Streptomyces coelicolor
 US-10-511-244-6

Query Match 56.2%; Score 1232.5; DB 5; Length 409;
 Best Local Similarity 57.1%; Pred. No. 1.2e-108;
 Matches 236; Conservative 54; Mismatches 118; Indels 5; Gaps 2;

Qy	1	MQSWSAIPAIVVPGRGAPALRLFDSADQVRPVTPPGTATMYCGITPYDATHLGHAAATYL 60
Db	1	MHAWPASEVPALPGQGRDLRIHDTATGGFVTLDPPGFVARIYVCGITPYDATHMGHAATYN 60
Qy	61	TFDLVHRLWLDAGHTVQVQNVTVDDPLFERAERDGDWRTGLDRETQLFREDMAALRV 120
Db	61	AFDLVQRVWLDTKRQVHYVQNVTVDDPLERARVDRDGVDTALAEQETALFREDMTALRM 120
Qy	121	LPVHDYVAATDAIAEVBWVEKLLASGAAYIVEDAEYDPVYFRADATAQPGYESGYDRDT 180
Db	121	LPVQHYIGAVEAIPGIVPLVERLDRDAGAAYELEG----DVYFSVBEADPHFGGVSHLDAAT 176
Qy	181	MLTLFAERGGDDPRPGKSDQDALLWRAERGPSPFGRGRPGHVECSAIALTRI 239
Db	177	MELLSAERGGDDPRPGKKNPLDPLMWAAREGEPSWDGGLGRGRPGWHIECVAILDHL 236
Qy	240	GTGLDIQGGSDLIIPHHYESAAHAEVYTGERRFAHYHTGMIGWDGKMSKSRGNLVL 299
Db	237	GMGFDVQGGSDLAFFPHHEMGASHAQAALTGEFPMAKAYHAGVMVLDGKMSKSGNLVF 296
Qy	300	VSOLRAQGVDPSPAIRLGLFSGHYREDRFSNEVLDEANARLARWR-SATALPEAPDATDVI 359
Db	297	VSQLRREGVDPSPAIRLTLAHLHYRSDWEWTDQVLDALRLDRWRAVSRPDGPPAEALV 356
Qy	360	AVRQYLDLDDTLPKALALDGCWCTDALSYGGHDTSPRLVATTVALLGVDL 412
Db	357	EBIREALANDLSPALAAVDRWAALQESGGTDDIGAPGVSVRAVDALLGVALL 409

RESULT 8
 US-10-511-244-5
 ; Sequence 5, Application US/10511244
 ; Publication No. US20060183116A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
 ; APPLICANT: SAREEN, Dipti
 ; APPLICANT: NEWTON, Gerald L.
 ; APPLICANT: FAHEY, Robert C.
 ; APPLICANT: BUCHMEIER, Nancy
 ; APPLICANT: STEFFEK, Micah
 ; APPLICANT: AV-GAY, Yossef
 ; APPLICANT: RAWAT, Mamta
 ; APPLICANT: KOLEDIN, Teresa
 ; TITLE OF INVENTION: METHODS OF USE OF THE ENZYMES OF MYCOTHOLIOL SYNTHESIS
 ; FILE REFERENCE: UCSD1420-1
 ; CURRENT APPLICATION NUMBER: US/10/511,244
 ; CURRENT FILING DATE: 2004-10-13
 ; PRIOR APPLICATION NUMBER: PCT/US 03/11539
 ; PRIOR FILING DATE: 2003-04-15
 ; PRIOR APPLICATION NUMBER: US 60/373,890
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: US 60/373,079
 ; PRIOR FILING DATE: 2002-04-15
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5

QY 299 LVSQRAQGVDPFAIRLGLFSGHYREDRFWSNEVLDEANARLWRSATAPPAADTV 358
 DB 301 LVSALRAQGVDPFAIRLGLFSGHYREDRFWSNEVLDEANARLWRSATAPPAADTV 360
 QY 359 IARVQYLADDDTPKALAAALGQWCTDALSYGGHDTSPRLVATTVDALLGVDL 412
 DB 361 VARVRYLADDDTPKALAAALGQWCTDALSYGGHDTSPRLVATTVDALLGVDL 414

RESULT 3

AG91416
 ID AAG91416 standard; protein; 404 AA.

AC AAG91416;

DT 15-JUN-2007 (revised)

DT 26-SEP-2001 (first entry)

DE C glutamicum protein fragment SEQ ID NO: 5170.

KW Corynebacterium; amino acid synthesis; vitamin; saccharide;
 KW organic acid synthesis; BOND_PC; CysteinyI-tRNA synthetase;
 KW CysteinyI-tRNA synthetase [Corynebacterium glutamicum ATCC 13032]; GO166;
 KW GO4812; GO4817; GO5524; GO6412; GO6423; GO16874.

XX Corynebacterium glutamicum.

XX EP1108790-A2.

XX 20-JUN-2001.

PF 18-DEC-2000; 2000EP-00127688.

PR 16-DEC-1999; 95UP-00377484.

PR 07-APR-2000; 2000JP-00159162.

PR 03-AUG-2000; 2000JP-00280988.

PA (KYOW) KYOWA HAKKO KOGYO KK.

XX Nakagawa S, Mizoguchi H, Ando S, Hayaishi M, Ochiai K, Yokoi H;

PI Tateishi N, Senoh A, Ikeda M, Ozaki A;

XX WPI; 2001-376931/40.

DR N-PSDB; AAH66835.

DR PC:NCBI; G161216674.

DR PC:SWISSPROT; Q8NQC4.

XX Novel polynucleotides derived from Coryneform bacteria, for identifying
 PT mutation point of a gene, measuring expression of a gene, analyzing
 PT expression profile or pattern of a gene and identifying homologous gene.

PS Claim 17; SEQ ID NO 5170; 246pp + Sequence Listing; English.

CC The present invention provides a number of nucleotide and protein
 CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of coryneform bacterium, measuring expression amount and analysing
 CC the expression profile or expression pattern of a gene derived from
 CC Coryneform bacterium, and identifying a homologue of a gene derived from
 CC coryneform bacterium. Coryneform bacteria are useful for producing amino
 CC acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a protein described in the
 CC exemplification of the invention. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from the European Patent Office

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.

SQ Sequence 404 AA;

Query Match 57.8%; Score 1269; DB 4; Length 404;
 Best Local Similarity 60.6%; Pred. No. 9.6e-119;

Matches 246; Conservative 45; Mismatches 99; Indels 16; Gaps 4;
 QY 19 LRLFDSDADQVRVPTFGPTAT-----MYVCGITPYDATHLGHAAATYLTEDLVHRLWLDAG 73
 DB 3 LELFDADQVRVPTFGPTAT-----MYVCGITPYDATHLGHAAATYLTEDLVHRLWLDAG 62
 QY 74 HTVQYVQNTVDVDDPLFERAERDGDWRTLGDRGTQTFREDMAALRVLPHPHYVAATDAI 133
 DB 63 HDVHYVQNTVDVDDPLFERAERDGDWRTLGDRGTQTFREDMAALRVLPHPHYVAATDAI 122
 QY 134 AEVVEVVEKLLASGAAYIVEDAEYPDVYFRADATAGFYSGYDRTDMLTLFAERGGPDD 193
 DB 123 DEVIEMVKLLDEGAAYIVEDAEYPDVYFRADATAGFYSGYDRTDMLTLFAERGGPDD 182
 QY 194 RPKGSDQLDALLWRAERPGCEPSPGRCGRPGHVECSAIALTRIGTGLDIQGGGSLI 253
 DB 183 RPKGNPMDALLWRAERPGCEPSPGRCGRPGHVECSAIALTRIGTGLDIQGGGSLI 242
 QY 254 FPHHEYSAAHAESVTGERPFARHYVHTGMIGWDHMKSKRGNLVLSQRAQGVDPFAI 313
 DB 243 FPHHEYSAAHAESVTGERPFARHYVHTGMIGWDHMKSKRGNLVLSQRAQGVDPFAI 302
 QY 314 RLGLFSGHYREDRFWSNEVLDEANARLWRSATAPPAADTVIARVQYLADDDTV 372
 DB 303 RLGVFANHYGRNDRMNAESLATAEQRLATWREAAATNREDAIAVVEQLRAHLSADLDT 362
 QY 373 PKALAAALDQWC-----TDALSYGGHDTSPRLVATTVDALLGVDL 412
 DB 363 PGALAAAVDNWAAGIDTTTDSKEP-----TEVGNIVVAIDAALLGVQL 404

RESULT 4

ABM79603

ID ABM79603 standard; protein; 409 AA.

XX AC ABM79603;

DT 15-JUN-2007 (revised)

DT 22-APR-2004 (first entry)

XX S coelicolor MshC protein.

XX Enzyme; mycothiol synthesis; MshC; MshD; MshA; infection;
 KW cysteine:glucosaminyl inositol ligase; antibacterial;
 KW acetyl-CoA:Cys-Gln-Ins acetyltransferase; BOND_PC;
 KW putative cysteinyI-tRNA synthetase;
 KW putative cysteinyI-tRNA synthetase [Streptomyces coelicolor A3(2)];
 KW SC152_05c; cysteinyI-tRNA synthetase;
 KW cysteinyI-tRNA synthetase [Streptomyces coelicolor A3(2)]; cyss; GO166;
 KW GO4812; GO4817; GO5524; GO6412; GO6423; GO16874.

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